Amendment to the Claims:

Please amend the claims as follows:

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A ~~high throughput~~ method of identifying a function of a polypeptide-encoding sequence of interest endogenously expressed by a cell type using high throughput detection comprising:

a) providing at least a first and a second pseudotyped lentiviral vector, each comprising a least a part of the polypeptide-encoding sequence of interest or a complementary sequence thereof, wherein the first lentiviral vector is designed to overexpress the endogenously expressed polypeptide-encoding sequence of interest and the second lentiviral vector is designed to inhibit or terminate expression of the endogenously expressed sequence of interest~~, and both the first and the second pseudotyped lentiviral vector can only express the at least part of the polypeptide-encoding sequence of interest or complementary sequence thereof~~;

b) providing a first and a second population of the cell type, and transducing the first lentiviral vector in the first cell population and transducing the second lentiviral vector in the second cell population;

c) overexpressing all or part of said polypeptide-encoding sequence in the first population of said cell type and inhibiting or terminating expression of said polypeptide-encoding sequence in the second population of said cell type;

d) high throughput detecting at least one change in one or more endogenous cellular factors in said first and second populations and comparing the effect on the cell of overexpression of the polypeptide-encoding sequence with the effect on the cell of inhibition or termination of expression of the polypeptide-encoding sequence; and

e) identifying a function of said polypeptide-encoding sequence of interest based on the detected and compared effect on the cell of overexpression and inhibition or termination of expression of said one or more cellular factors.

Claim 2 (previously presented): The method of claim 1 wherein said at least one change is an increase and/or decrease in the expression of said endogenous cellular factors.

Claim 3 (previously presented): The method of claim 1 wherein said at least one change is in a post-translational modification of said endogenous cellular factors.

Claim 4 (previously presented): The method of claim 3 wherein said post-translational modification comprises a phosphorylation or glycosylation of said cellular factors.

Claim 5 (previously presented): The method of claim 1 wherein said at least one change is in an activity of said cellular factors.

Claim 6 (previously presented): The method of claim 1 wherein said pseudotyped lentiviral vector is a conditionally replicating pseudotyped lentiviral vector.

Claim 7 (previously presented): The method of claim 1 wherein said inhibiting expression of said polypeptide-encoding sequence in a second population is by use of a pseudotyped lentiviral vector capable of expressing all or part of said polypeptide-encoding sequence in an antisense orientation.

Claim 8 (previously presented): The method of claim 1 wherein said inhibiting or terminating expression of said polypeptide-encoding sequence in a second population is by use of a pseudotyped lentiviral vector capable of expressing one or more ribozymes against said polypeptide-encoding sequence.

Claim 9 (previously presented): The method of claim 1 wherein said inhibiting or terminating expression of said polypeptide-encoding sequence in a second population is by the generation of post-transcriptional gene silencing (PTGS) against said polypeptide-encoding sequence.

Claim 10 (original): The method of claim 1 wherein said cell type is a primary cell.

Claims 11 to 13 (canceled)

Claim 14 (previously presented): The method of claim 1 wherein said polypeptide-encoding sequence of interest encodes a product which modulates expression of said one or more cellular factors by binding to nucleic acids encoding, or regulating the expression of, said one or more cellular factors.

Claim 15 (previously presented): The method of claim 12 wherein said polypeptide-encoding sequence of interest encodes a transcriptional activator.

Claim 16 (previously presented): The method of claim 12 wherein said polypeptide-encoding sequence of interest encodes a transcriptional repressor.

Claim 17 (previously presented): The method of claim 1 wherein said polypeptide-encoding sequence of interest is a human sequence.

Claim 18 (previously presented): The method of claim 1 wherein said cell type is a human, a plant or a microorganism cell type.

Claim 19 (previously presented): A method of altering the expression of one or more cellular factors in a cell comprising overexpressing or inhibiting the expression of a gene sequence for which a function was identified by the method of claim 1.

Claim 20 (previously presented): A method of altering the phenotype of a cell comprising overexpressing or inhibiting the expression of a gene sequence for which a function was identified by the method of claim 1.

Claim 21 (currently amended): A ~~high throughput~~ method of identifying a function of a gene sequence of interest in a cell heterologous to the cellular source of said gene sequence using high throughput detection comprising:

a) providing at least a first and a second pseudotyped lentiviral vector, each comprising a least a part of the gene sequence of interest or a complementary sequence thereof,

wherein the first lentiviral vector is designed to overexpress the expressed gene sequence of interest and the second lentiviral vector is designed to underexpress or terminate the expressed sequence of interest, and overexpression and underexpression or termination is relative to the level of expression of the gene sequence in the cell from which the gene sequence was derived~~, and both the first and the second pseudotyped lentiviral vector can only express the at least part of the gene sequence of interest or complementary sequence thereof~~;

(b) providing a first and a second population of the cell, and transducing the first lentiviral vector in a first cell population and transducing the second lentiviral vector in a second cell population;

(c) overexpressing all or part of said gene sequence in the first population of said cell and inhibiting or terminating expression of said sequence in a second population of said cell type;

(d) high throughput detecting at least one change in one or more cellular factors in said first and second populations and comparing the effect on the cell of overexpression of the gene sequence with the effect on the cell of inhibition or termination of expression of the gene sequence; and

(e) identifying a function of said gene sequence of interest based on the detected and compared effect on the cell of overexpression and inhibition or termination of expression of said one or more cellular factors.

Claim 22 (currently amended): A method of detecting <u>using high throughput detection</u> a change in one or more cellular factors in a cell due to the overexpression or inhibition of a gene sequence of interest in said cell, comprising:

a) providing at least a first and a second pseudotyped lentiviral vector, each comprising a least a part of the gene sequence of interest or a complementary sequence thereof,

wherein the first lentiviral vector is designed to overexpress the expressed gene sequence of interest and the second lentiviral vector is designed to underexpress or terminate the expressed sequence of interest, and overexpression and underexpression or termination is relative to the level of expression of the gene sequence in the cell from which the gene sequence was derived~~, and both the first and the second pseudotyped lentiviral vector can only express the at least part of the gene sequence of interest or complementary sequence thereof~~;

(b) providing a first and a second population of the cell, and transducing the first lentiviral vector in a first cell population and transducing the second lentiviral vector in a second cell population;

(c) overexpressing all or part of said gene sequence in the first population of said cell type and inhibiting expression of said gene sequence in a second population of said cell type; and

(d) high throughput detecting at least one change in one or more cellular factors in said first and second populations by comparing the effect on the cell of overexpression of the gene sequence with the effect on the cell of inhibition or termination of expression of the gene sequence.

Claim 23 (previously presented): The method of claim 22, further comprising a step:

(e) identifying the function of said gene sequence of interest based on the detected and compared effect on the cell of overexpression and inhibition or termination of expression of said one or more cellular factors.

Claim 24 (previously presented): The method of claim 23, further comprising a step:

(f) altering the expression of said one or more cellular factors in a third population of said cell type cell by overexpressing or inhibiting the expression of said gene of interest for which a function was identified in step (e).

Claim 25 (previously presented): The method of claim 23, further comprising a step:

(f) altering the phenotype of a third population of said cell type by overexpressing or inhibiting the expression of said gene sequence of interest for which a function was identified in step (e).

Claim 26 (previously presented): The method of claim 22, wherein said cell is heterologous to the cellular source of said gene sequence of interest, and overexpression and underexpression or terminate is relative to the level of expression of the gene sequence in the cell from which the gene sequence was derived.

Claim 27 (previously presented): The method of claim 22, wherein said cellular factor comprises a cellular gene product or a metabolite.

Claim 28 (previously presented): The method of claim 27, wherein said cellular gene product comprises a protein or RNA.

Claim 29 (previously presented): The method of claim 27, wherein said metabolite comprises a sugar or a lipid.

Claim 30 (previously presented): The method of claim 1, wherein inhibiting or terminating expression of the polypeptide-encoding sequence is mediated by post-transcriptional gene silencing (PTGS), small interfering RNA (siRNA), RNA interference, or an antisense or a ribozyme sequence targeted against the polypeptide-encoding sequence.

Claim 31 (previously presented): The method of claim 1, wherein the high throughput detecting comprises use of computerized or robot implemented systems.

Claim 32 (previously presented): The method of claim 31, wherein the high throughput detecting comprises use of libraries of lentiviral vectors and cells transduced by the lentiviral vectors.

Claim 33 (previously presented): The method of claim 32, wherein the high throughput detecting comprises use of libraries of lentiviral vectors and cells transduced by the lentiviral vectors in a multiplicity of compartments.

Claim 34 (previously presented): The method of claim 1, wherein the high throughput detecting comprises use of machine implemented microarray or macroarray technology.

Claim 35 (previously presented): The method of claim 21, wherein inhibiting or terminating expression of the gene sequence is mediated by post-transcriptional gene silencing (PTGS), small interfering RNA (siRNA), RNA interference, or an antisense or a ribozyme sequence targeted against the polypeptide-encoding sequence.

Claim 36 (previously presented): The method of claim 21, wherein the high throughput detecting comprises use of computerized or robot implemented systems.